

#6  
8/23/00  
SK

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AUG 15 2000

TECH CENTER 1600/2900

1643

ENTERED

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/503,089A DATE: 08/09/2000  
 TIME: 15:22:36

Input Set : A:\09503089.app  
 Output Set: N:\CRF3\08092000\I503089A.raw

3 <110> APPLICANT: PATEL, AMANDA J.  
 4 HONORE, ERIC  
 5 LESAGE, FLORIAN  
 6 ROMEY, GEORGES  
 7 LAZDUSKI, MICHEL  
 9 <120> TITLE OF INVENTION: A method for the identification of anesthetics  
 11 <130> FILE REFERENCE: f17b12prov3-humanTREK  
 13 <140> CURRENT APPLICATION NUMBER: 09/503,089A  
 14 <141> CURRENT FILING DATE: 2000-02-11  
 16 <160> NUMBER OF SEQ ID NOS: 5  
 18 <170> SOFTWARE: Microsoft Word 2000  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 1236  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (1)..(1236)  
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 31 Met Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser  
 32 1 5 10 15  
 34 aaa ccg agg ctc tcg ttt tcc acg aaa ccc aca gtg ctt gct tcc cg 96  
 35 Lys Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg  
 36 20 25 30  
 38 gtg gag agt gac acc att aat gtt atg aaa tgg aag acc gtc tcc 144  
 39 Val Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser  
 40 35 40 45  
 42 acg ata ttc ctg gtg gtt gtc ctc tat ctg atc atc gga gcc acc gtg 192  
 43 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val  
 44 50 55 60  
 46 ttc aaa gca ttg gag cag cct cat gag att tca cag agg acc acc att 240  
 47 Phe Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile  
 48 65 70 75 80  
 50 gtg atc cag aag caa aca ttc ata tcc caa cat tcc tgt gtc aat tcg 288  
 51 Val Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser  
 52 85 90 95  
 54 acg gag ctg gat gaa ctc att cag caa ata gtg gca gca ata aat gca 336  
 55 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala  
 56 100 105 110  
 58 ggg att ata ccg tta gga aac acc tcc aat caa atc agt cac tgg gat 384  
 59 Gly Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp  
 60 115 120 125  
 62 ttg gga agt tcc ttc ttc ttt gct ggc act gtt att aca acc ata gga 432  
 63 Leu Gly Ser Ser Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly  
 64 130 135 140  
 65 ttt gga aac atc tca cca cgc aca gaa ggc ggc aaa ata ttc tgt atc 480

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66 Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile  
67 145 150 155 160  
69 atc tat gcc tta ctg ggaa att ccc ctc ttt ggt ttt ctc ttg gct gga 528  
70 Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly  
71 165 170 175  
73 gtt gga gat cag cta ggc acc ata ttt gga aaa gga att gcc aaa gtg 576  
74 Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val  
75 180 185 190  
77 gaa gat acg ttt att aag tgg aat gtt agt cag acc aag att cgc atc 624  
78 Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile  
79 195 200 205  
81 atc tca aca atc ata ttt ata cta ttt ggc tgt gta ctc ttt gtg gct 672  
82 Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala  
83 210 215 220  
85 ctg cct gcg atc ata ttc aaa cac ata gaa ggc tgg agt gcc ctg gac 720  
86 Leu Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp  
87 225 230 235 240  
89 gcc att tat ttt gtg gtt atc act cta aca act att gga ttt ggt gac 768  
90 Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp  
91 245 250 255  
93 tac gtt gca ggt gga tcc gat att gaa tat ctg gac ttc tat aag cct 816  
94 Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro  
95 260 265 270  
97 gtc gtg tgg ttc tgg atc ctt gta ggg ctt gct tac ttt gct gtc 864  
98 Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val  
99 275 280 285  
101 ctg agc atg att gga gat tgg ctc cga gtg ata tct aaa aag aca aaa 912  
102 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys  
103 290 295 300  
105 gaa gag gtg gga gag ttc aga gca cac gct gct gag tgg aca gcc aac 960  
106 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn  
107 305 310 315 320  
109 gtc aca gcc gaa ttc aaa gaa acc agg agg cga ctg agt gtg gag att 1008  
110 Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile  
111 325 330 335  
113 tat gac aag ttc cag cgg gcc acc tcc atc aag cgg aag ctc tcg gca 1056  
114 Tyr Asp Lys Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala  
115 340 345 350  
117 gaa ctg gct gga aac cac aat cag gag ctg act cct tgt agg agg acc 1104  
118 Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr  
119 355 360 365  
121 ctg tca gtg aac cac ctg acc aac gag agg gat gtc ttg cct ccc tta 1152  
122 Leu Ser Val Asn His Leu Thr Asn Glu Arg Asp Val Leu Pro Pro Leu  
123 370 375 380  
125 ctg aag act gag agt atc tat ctg aat ggt ttg acg cca cac tgt gct 1200  
126 Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala  
127 385 390 395 400  
129 ggt gaa gag att gct gtg att gag aac atc aaa tag 1236  
130 Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys

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Input Set : A:\09503089.app  
 Output Set: N:\CRF3\08092000\I503089A.raw

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131      405          410
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 411
136 <212> TYPE: PRT
137 <213> ORGANISM: Homo sapiens ✓
139 <400> SEQUENCE: 2
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143     20          25          30
144 Val Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser
145     35          40          45
146 Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val
147     50          55          60
148 Phe Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile
149     65          70          75          80
150 Val Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser
151     85          90          95
152 Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala
153     100         105         110
154 Gly Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp
155     115         120         125
156 Leu Gly Ser Ser Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly
157     130         135         140
158 Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile
159     145         150         155         160
160 Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly
161     165         170         175
162 Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val
163     180         185         190
164 Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile
165     195         200         205
166 Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala
167     210         215         220
168 Leu Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp
169     225         230         235         240
170 Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp
171     245         250         255
172 Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro
173     260         265         270
174 Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val
175     275         280         285
176 Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr Lys
177     290         295         300
178 Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn
179     305         310         315         320
180 Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile
181     325         330         335
182 Tyr Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala

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183      340      345      350
184 Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr
185      355      360      365
186 Leu Ser Val Asn His Leu Thr Asn Glu Arg Asp Val Leu Pro Pro Leu
187      370      375      380
188 Leu Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Thr Pro His Cys Ala
189 385      390      395      400
190 Gly Glu Glu Ile Ala Val Ile Glu Asn Ile Lys
191      405      410
194 <210> SEQ ID NO: 3
195 <211> LENGTH: 3580
196 <212> TYPE: DNA
197 <213> ORGANISM: Mus musculus
199 <220> FEATURE:
200 <221> NAME/KEY: CDS /
201 <222> LOCATION: (484)..(1719)
203 <400> SEQUENCE: 3
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208 gaagaggggc tgcatgtatc accccccttcgc tgagccccgg ggcagagccc agccggccgc 180
210 cgagccgcacg gaggccacggg ccgacgcac ccaggccggg cgcgggaccc caggccggcca 240
212 cgcacatccggg gtgacccatc gcgcgcgggg gcgtcgctgt ccgcattccaa ctggccctcg 300
214 gcctcgccct ctgcccacggc tgccaccgcgt ggtgtccctt ccttccggg atttcgtttc 360
216 ttctcacgtt ccccccctta tacccttccc gcctccagcc cgcgtctccc caccttgata 420
218 aacaagccg gggaaaatgc ctacccgtgc agctcgggac ggcagcccg tcttggata 480
220 agg`atg gcg gcc cct gac ttg ctg gat ccc aag tct gct gtc gat cag aac 528
221     Met Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn
222      1          5          10          15
224 tcc aaa ccg agg ctc tca ttc tcc tca aaa ccc acc gtg ctt gct tcc 576
225 Ser Lys Pro Arg Leu Ser Phe Ser Ser Lys Pro Thr Val Leu Ala Ser
226      20          25          30
228 cgg gtg gag agt gac tcg gcc att aat gtt atg aaa tgg aag aca gtc 624
229 Arg Val Glu Ser Asp Ser Ala Ile Asn Val Met Lys Trp Lys Thr Val
230      35          40          45
232 tcc acg att ttc ctg gtg gtc gtc ctc tac ctg atc atc gga gcc gcg 672
233 Ser Thr Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Ala
234      50          55          60
236 gtg ttc aag gca ttg gag cag cct cag gag att tcc cag agg acc acc 720
237 Val Phe Lys Ala Leu Glu Gln Pro Gln Glu Ile Ser Gln Arg Thr Thr
238      65          70          75
240 att gtg atc cag aag cag acc ttc ata gcc cag cat gcc tgc gtc aac 768
241 Ile Val Ile Gln Lys Gln Thr Phe Ile Ala Gln His Ala Cys Val Asn
242      80          85          90          95
244 tcc acc gag ctg gac gaa ctc atc cag caa ata gtg gca gca ata aac 816
245 Ser Thr Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ile Asn
246      100         105         110
248 gca ggg att atc ccc tta gga aac agc tcc aat caa gtt agt cac tgg 864
249 Ala Gly Ile Ile Pro Leu Gly Asn Ser Ser Asn Gln Val Ser His Trp
250      115         120         125

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252 gac ctc gga agc tct ttc ttc gtc ggt act gtt atc aca acc ata	912
253 Asp Leu Gly Ser Ser Phe Phe Ala Gly Thr Val Ile Thr Thr Ile	
254 130 135 140	
255 gga ttt gga aac atc tcc cca cga act gaa ggt gga aaa ata ttc tgc	960
257 Gly Phe Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys	
258 145 150 155	
260 atc atc tat gcc ttg ctg gga att ccc ctc ttt ggc ttt cta ctg gct	1008
261 Ile Ile Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala	
262 160 165 170 175	
264 ggg gtt ggt gat cag cta gga act ata ttt gga aaa gga att gcc aaa	1056
265 Gly Val Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys	
266 180 185 190	
268 gtg gaa gac aca ttt att aag tgg aat gtt agt cag acg aag att cgt	1104
269 Val Glu Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg	
270 195 200 205	
272 atc atc tcc acc atc atc ttc atc ctg ttt ggc tgt gtc ctc ttt gtg	1152
273 Ile Ile Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val	
274 210 215 220	
276 gct ctc cct gcg gtc ata ttc aag cac ata gaa ggc tgg acg gcc ctg	1200
277 Ala Leu Pro Ala Val Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu	
278 225 230 235	
280 gac gct atc tat ttt gtg gtt atc act ctg acg acc att gga ttt gga	1248
281 Asp Ala Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly	
282 240 245 250 255	
284 gac tac gtg gca ggt gga tca gac att gaa tat ctg gac ttc tac aag	1296
285 Asp Tyr Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys	
286 260 265 270	
288 cct gtg gtg tgg ttc tgg atc ctc gtt ggg ctg gcc tac ttt gca gct	1344
289 Pro Val Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala	
290 275 280 285	
292 gtt ctg agc atg att ggg gac tgg cta cgg gtg atc tct aag aag acg	1392
293 Val Leu Ser Met Ile Gly Asp Trp Leu Arg Val Ile Ser Lys Lys Thr	
294 290 295 300	
296 aag gaa gag gtg gga gag ttc aga gcg cat gcc gct gag tgg aca gcc	1440
297 Lys Glu Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala	
298 305 310 315	
300 aat gtc acg gcc gag ttc aag gaa acg agg cgg ctg agc gtg gag	1488
301 Asn Val Thr Ala Glu Phe Lys Glu Thr Arg Arg Leu Ser Val Glu	
302 320 325 330 335	
304 atc tac gac aag ttc cag cgt gcc aca tcc gtg aag cgg aag ctc tcc	1536
305 Ile Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser	
306 340 345 350	
308 gca gag ctg gcg ggc aac cac aac cag gaa ctg act ccg tgt agg agg	1584
309 Ala Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg	
310 355 360 365	
312 acc ctg tct gtg aac cac ctg acc agc gag agg gaa gtc ctg cct ccc	1632
313 Thr Leu Ser Val Asn His Leu Thr Ser Glu Arg Glu Val Leu Pro Pro	
314 370 375 380	
316 ttg ctg aag gct gag agc atc tat ctg aac ggt ctg aca cca cac tgt	1680

**VERIFICATION SUMMARY** DATE: 08/09/2000  
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Input Set : A:\09503089.app  
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